UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/867,570	05/31/2001	Ming-Hui Wei	CL000900CIP	8055

25748 7590 01/24/2005

CELERA GENOMICS CORP.
ATTN: WAYNE MONTGOMERY, VICE PRES, INTEL PROPERTY
45 WEST GUDE DRIVE
C2-4#20
ROCKVILLE, MD 20850

EXAMINER	
LOCKARD, JON MCCLELLAND	
ART UNIT	PAPER NUMBER
1647	

DATE MAILED: 01/24/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/867,570	WEI ET AL.	
	Examiner	Art Unit	
	Jon M Lockard	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *23 September 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *4,8,9,12 and 24-29* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *4, 8-9, 12, and 24-29* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *7/1/02, 9/23/04*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *Sequence ALignments*.

DETAILED ACTION

Election/Restrictions

1. Applicant's election of Group III, claims 4-5, 8-11, and 22-23 drawn to nucleic acids of SEQ ID NOs:2 and 3, vectors and host cells comprising the same, and a method of recombinantly producing the polypeptide of SEQ ID NO:2, in the reply filed on 23 September 2004 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

2. The restriction requirement is still deemed proper and is therefore made FINAL.

Status of Application, Amendments, And/Or Claims

3. Applicants' amendment filed on 23 September 2004 has been received and entered in full. Claims 1-3, 5-7, and 10-23 have been cancelled, claims 4 and 8-9 have been amended, and claims 24-29 have been added. Claims 4, 8-9, and 24-29 are currently pending.

Information Disclosure Statement

4. The Information Disclosure Statements (IDS) submitted on 01 July 2002 and 23 September 2004 have been considered by the Examiner. The BLAST results submitted on 23 September 2004 demonstrate that applicants are aware of proteins with identity/homology to the one claimed herein. However, as the BLAST results do not give sufficient identifying information, the Examiner cannot determine if said sequences constitute prior art.

Claim Rejections - 35 USC § 101 and 35 USC §112

5. 35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.
>
> The following is a quotation of the first paragraph of 35 U.S.C. 112:
>
> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

6. Claims 4, 8-9, and 24-29 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific, substantial, and credible asserted utility or a well established utility. Novel biological molecules lack an established utility and must undergo extensive experimentation to determine an appropriate specific, substantial, and credible utility.

7. The instant application discloses a nucleic acid set forth as SEQ ID NO:1 (transcript) and SEQ ID NO:3 (genomic) that encodes the protein set forth as SEQ ID NO:2, and vectors and host cells comprising the same. The specification asserts that SEQ ID NO:2 is a G protein coupled receptor (GPCR) that is related to the human Mas-related GPCR subfamily based on a high degree of homology to known GPCR sequences (See page 11, line 10-12; Figure 1). The Specification also discloses that the nucleic acid encoding SEQ ID NO:2 is expressed in human erythroleukemia cells and testis (See page 11, lines 19-20; Figure 1). The instant specification does not teach any physiologic ligands or functional characteristics of the GPCR set forth in SEQ ID NO:2 or encoded by the disclosed nucleic acid set forth in SEQ ID NOs:1 and 3. There is no

well-established utility for a specific nucleic acid or amino acid sequence and the specification fails to disclose a specific and substantial utility for the claimed invention.

8. The specification asserts the following as patentable utilities for the claimed DNA (SEQ ID NOs:1 and 3) encoding the receptor protein of SEQ ID NO:2:

1) as hybridization probes and PCR primers (pg 41, lines 7 and 13-19; pg 42, lines 13-24);

2) recombinant production of the encoded protein (pg 41, lines 20-28);

3) chromosome mapping (pg 41, line 29 – pg 42, line 32);

4) designing ribozymes (pg 42, lines 5-6);

5) production of transgenic non-human animals (pg 42, lines 11-12);

6) diagnostic kits (pg 42, line 28 – pg 43, line 3);

7) drug screening assays to identify compounds that modulate nucleic acid expression (pg 43, lines 4-5);

8) methods of monitoring treatment (pg 44, lines 17-26);

9) diagnostic assays (pg 44, line 27 – pg 46, line 21);

10) pharmacogenomics (pg 46, lines 22-28);

11) antisense constructs (pg 47, lines 3-16);

12) gene therapy (pg 47, lines 17-21);

13) kits for nucleic acid detection (pg 47, line 22 – pg 48, line 2); and

14) useful in arrays (pg 48, line 5 – pg 50, line 13).

9. These asserted utilities are neither specific nor substantial because they do not identify or reasonably confirm a "real world" context of use. The specification neither identifies the biological functions of the claimed protein and DNA, nor any diseases that are associated with the claimed molecules. Without any biological activity or link to a disease, such constitutes

further research to determine the properties of the claimed GPCR protein or partial peptides, which is insufficient to meet the requirement of 35 USC § 101.

10. These activities and functions are conjectural and are based solely on the identification of the putative protein of SEQ ID NO:2 as being a G-protein coupled receptor (GPCR). While it is credible that SEQ ID NO:2 is a GPCR, its identification as such is not sufficient to establish either a well known, or a specific, substantial and credible utility. There is no ligand identified that binds to it, no signaling pathway with which it is involved, and no disease or disorder correlated with the polypeptide. In Tables 3-5 it is disclosed that the nucleic acid is expressed in a variety of cell lines and tissues. The Specification discloses that the nucleic acid is expressed in human erythroleukemia cells and testis. The Instant Application has not provided sufficient experimental data to establish a nexus between the expression of the nucleic acid of SEQ ID NOs:1 and 3 and any disease or disorder. Since the instant specification does not disclose how to use the polypeptide of SEQ ID NO:2, a skilled artisan would not know how to use nucleic acids of SEQ ID NO:1 and 3 that encode the polypeptide.

11. The art teaches that the GPCR family is extremely diverse, and that function cannot be predicted merely by identifying a protein as a GPCR. For example, Ji et al., in the Journal of Biological Chemistry 273(28): 17299-17302, teach that there have been nearly 2000 GPCR's reported, which are classifiable into 100 sub families according to sequence homology, ligand structure and receptor function. They further teach that different GPCR superfamily members are capable of sending signals via alternative signal molecules such as Jak2, phospholipase C, or protein kinase C, and that there are other seven transmembrane domain molecules that are not coupled to G proteins at all. Marchese et al. (Genomics 29:335), teach that IL-8 receptor,

neuropeptide Y receptor and Somatostatin receptors are all GPCR's. Thus, although the homology of the GPCR family, especially in the transmembrane domain regions, allows identification of such as GPCRs, mere homology and quantification of gene expression is not accepted by those of skill in the art as being predictive of function. Utility must be in readily available form. It is possible that, after further characterization, this protein might be found to have a patentable utility, in which case proteins would have a specific utility, or the protein might be found to be associated with a specific disease.

12. In Brenner v. Manson, 148 U.S.P.Q. 689 (Sup. Ct., 1966), a process of producing a novel compound that was structurally analogous to other compounds which were known to possess anti-cancer activity was alleged to be useful because the compound produced thereby was potentially useful as an anti-tumor agent in the absence of evidence supporting this utility. The court expressed the opinion that all chemical compounds are "useful" to the chemical arts when this term is given its broadest interpretation. However, the court held that this broad interpretation was not the intended definition of "useful" as it appears in 35 U.S.C. § 101, which requires that an invention must have either an immediately obvious or fully disclosed "real world" utility. The instant claims are drawn to a protein which has undetermined function or biological significance. Until some actual and specific activity or significance can be attributed to the protein identified in the specification as SEQ ID NO:2 or the polynucleotide encoding it (SEQ ID NOs:1 and 3), the claimed invention is incomplete.

13. Claims 4, 8-9, and 24-29 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific, substantial and

credible asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to make/use the claimed invention.

Summary

14. No claim is allowed.

15. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure.

16. Ahmad et al. (US Pat. No. 6,696,257) teach a nucleic acid (SEQ ID NO:4) that encodes a protein that shares 99% sequence identity with amino acid residues 16-337 of SEQ ID NO:2 of the Instant Application (See attached sequence alignment).

17. Chen et al. (US Application No. US20020193584 A1) teach a nucleic acid (SEQ ID NO:19) that encodes a protein that shares 100% sequence identity with amino acid residues 16-337 of SEQ ID NO:2 of the Instant Application (See attached sequence alignment).

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to **Jon M. Lockard, Ph.D.** whose telephone number is **(571) 272-2717**. The examiner can normally be reached on Monday through Friday, 8:00 AM to 6:00 PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, **Brenda Brumback, Ph.D.** can be reached on **(571) 272-0961**.

The fax number for the organization where this application or proceeding is assigned is **703-872-9306**.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see **http://pair-direct.uspto.gov**. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at **866-217-9197** (toll-free).

JML
January 10, 2005

Lorraine Spector

LORRAINE SPECTOR
PRIMARY EXAMINER

Sequence Alignments

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 1, 2004, 22:49:23 ; Search time 107 Seconds
(without alignments)
2238.653 Million cell updates/sec

Title: US-09-867-570-2
Perfect score: 1763
Sequence: 1 MESKSSWVIRLGFLSMDSTI.....EGGGWLPQETLELSGSRLEQ 337

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09867570/runat_01122004_161123_6373/app_query.fasta_1.519
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09867570_@CGN_1_1_105_@runat_01122004_161123_6373 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1642	93.1	969	4	US-09-254-227A-4	Sequence 4, Appli
2	1598	90.6	969	4	US-09-254-227A-6	Sequence 6, Appli
3	1405	79.7	969	4	US-09-254-227A-8	Sequence 8, Appli
4	1382	78.4	969	4	US-09-254-227A-10	Sequence 10, Appl
5	1382	78.4	969	4	US-09-254-227A-12	Sequence 12, Appl
6	1360	77.1	969	4	US-09-254-227A-14	Sequence 14, Appl
7	834.5	47.3	1011	4	US-09-254-227A-2	Sequence 2, Appli
8	529	30.0	291	4	US-09-495-050A-164	Sequence 164, App
9	496	28.1	275	4	US-09-016-434-330	Sequence 330, App
10	461	26.1	2416	4	US-09-016-434-1264	Sequence 1264, Ap
11	430.5	24.4	1388	4	US-09-016-434-1225	Sequence 1225, Ap
12	430.5	24.4	1388	5	PCT-US93-06251-26	Sequence 26, Appl
13	392.5	22.3	1327	6	5320941-1	Patent No. 5320941
14	381.5	21.6	2435	4	US-09-484-970B-134	Sequence 134, App
15	255.5	14.5	2911	3	US-08-981-825-5	Sequence 5, Appli
16	255.5	14.5	2911	3	US-09-480-784-5	Sequence 5, Appli
17	240	13.6	1200	5	PCT-US95-03032-1	Sequence 1, Appli
18	238	13.5	1062	4	US-09-016-434-1207	Sequence 1207, Ap
19	231	13.1	1200	5	PCT-US92-02977-1	Sequence 1, Appli
20	227.5	12.9	1106	5	PCT-US92-02977-5	Sequence 5, Appli
21	227.5	12.9	1106	5	PCT-US95-03032-4	Sequence 4, Appli
22	226.5	12.8	1510	1	US-07-759-568-4	Sequence 4, Appli
23	226.5	12.8	1510	4	US-09-023-655-1140	Sequence 1140, Ap
24	226.5	12.8	1748	1	US-08-202-056-8	Sequence 8, Appli
25	226.5	12.8	1750	4	US-09-023-655-1135	Sequence 1135, Ap
26	225.5	12.8	1143	1	US-08-467-125-1	Sequence 1, Appli
27	225.5	12.8	1143	2	US-08-911-320A-1	Sequence 1, Appli
28	225.5	12.8	1143	3	US-09-217-101-1	Sequence 1, Appli
29	225.5	12.8	1842	4	US-09-016-434-46	Sequence 46, Appl
30	220	12.5	1244	1	US-07-816-283-7	Sequence 7, Appli
31	220	12.5	1244	1	US-08-417-103-7	Sequence 7, Appli
32	220	12.5	1373	5	PCT-US92-02977-6	Sequence 6, Appli
33	220	12.5	1373	5	PCT-US95-03032-3	Sequence 3, Appli
34	217	12.3	1058	4	US-09-016-434-1206	Sequence 1206, Ap
35	217	12.3	1910	4	US-09-944-807-1	Sequence 1, Appli
36	217	12.3	2631	4	US-09-023-655-1083	Sequence 1083, Ap
37	214.5	12.2	1317	4	US-09-016-434-1446	Sequence 1446, Ap
38	214	12.1	1438	4	US-09-016-434-1426	Sequence 1426, Ap
39	211	12.0	1062	4	US-09-576-160B-12	Sequence 12, Appl
40	210	11.9	1068	4	US-09-170-496D-1	Sequence 1, Appli
41	206	11.7	1068	4	US-09-170-496D-163	Sequence 163, App
42	205.5	11.7	1289	4	US-09-745-842-1	Sequence 1, Appli
43	205	11.6	1002	4	US-09-170-496D-7	Sequence 7, Appli
44	205	11.6	1265	4	US-09-016-434-1430	Sequence 1430, Ap
45	204	11.6	1002	4	US-09-170-496D-167	Sequence 167, App

ALIGNMENTS

RESULT 1
US-09-254-227A-4
; Sequence 4, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
; APPLICANT: Ahmad, Sultan
; APPLICANT: Banville, Denis
; APPLICANT: Fortin, Yves
; APPLICANT: Lembo, Paola
; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/09/254,227A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-254-227A-4

Alignment Scores:

Pred. No.:	1.87e-157	Length:	969
Score:	1642.00	Matches:	313
Percent Similarity:	98.76%	Conservative:	5
Best Local Similarity:	97.20%	Mismatches:	4
Query Match:	93.14%	Indels:	0
DB:	4	Gaps:	0

US-09-867-570-2 (1-337) x US-09-254-227A-4 (1-969)

```
Qy         16 MetAspSerThrIleProValLeuGlyThrGluLeuThrProIleAsnGlyArgGluGlu 35
              ||||||  ||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db          1 ATGGATCCAACCATCCCAGTCTTGGGTACAAAACTGACACCAATCAACGGACGTGAGGAG 60
```

```
Qy         36 ThrProCysTyrLysGlnThrLeuSerPheThrGlyLeuThrCysIleValSerLeuVal 55
              ||||||||||||   |||||||||||||||||||||||||||||:::|||||||||
Db         61 ACTCCTTGCTACAACCAAACCCTGAGCTTCACGGGGCTGACGTGCATCATTTCCCTTGTC 120

Qy         56 AlaLeuThrGlyAsnAlaValValLeuTrpLeuLeuGlyCysArgMetArgArgAsnAla 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTGCCGCATGCGCAGGAACGCT 180

Qy         76 ValSerIleTyrIleLeuAsnLeuValAlaAlaAspPheLeuPheLeuSerGlyHisIle 95
              ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db        181 GTCTCCATCTACATCCTCAACCTGGTCGCGGCCAACTTCCTCTTCCTTAGCGGCCACATT 240

Qy         96 IleCysSerProLeuArgLeuIleAsnIleArgHisProIleSerLysIleLeuSerPro 115
              |||  |||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        241 ATATTTTCGCCGTTACCCCTCATCAATATCCGCCATCCCATCTCCAAAATCCTCAGTCCT 300

Qy        116 ValMetThrPheProTyrPheIleGlyLeuSerMetLeuSerAlaIleSerThrGluArg 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGATGACCTTTCCCTACTTTATAGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGC 360

Qy        136 CysLeuSerIleLeuTrpProIleTrpTyrHisCysArgArgProArgTyrLeuSerSer 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCGCCCCAGATACCTGTCATCG 420

Qy        156 ValMetCysValLeuLeuTrpAlaLeuSerLeuLeuArgSerIleLeuGluTrpMetPhe 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCATGTGTGTCCTGCTCTGGGCCCTGTCCCTGCTGCGGAGTATCCTGGAGTGGATGTTC 480

Qy        176 CysAspPheLeuPheSerGlyAlaAspSerValTrpCysGluThrSerAspPheIleThr 195
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db        481 TGTGACTTCCTGTTTAGTGGTGCTAATTCTGTTTGGTGTGAAACGTCAGATTTCATTACA 540

Qy        196 IleAlaTrpLeuValPheLeuCysValValLeuCysGlySerSerLeuValLeuLeuVal 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCGCGTGGCTGGTTTTTTTATGTGTGGTTCTCTGTGGGTCCAGCCTGGTCCTGCTGGTC 600

Qy        216 ArgIleLeuCysGlySerArgLysMetProLeuThrArgLeuTyrValThrIleLeuLeu 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCCTCCTC 660

Qy        236 ThrValLeuValPheLeuLeuCysGlyLeuProPheGlyIleGlnTrpAlaLeuPheSer 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACAGTGCTGGTCTTCCTCCTCTGTGGCCTGCCCTTTGGCATTCAGTGGGCCCTGTTTTCC 720

Qy        256 ArgIleHisLeuAspTrpLysValLeuPheCysHisValHisLeuValSerIlePheLeu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTTCCATTTTCCTG 780

Qy        276 SerAlaLeuAsnSerSerAlaAsnProIleIleTyrPhePheValGlySerPheArgGln 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCCGCTCTTAACAGCAGTGCCAACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG 840

Qy        296 ArgGlnAsnArgGlnAsnLeuLysLeuValLeuGlnArgAlaLeuGlnAspThrProGlu 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGTCAAAATAGGCAAAACCTGAAGCTGGTTCTCCAAAGGGCTCTGCAGGACACGCCTGAG 900

Qy        316 ValAspGluGlyGlyGlyTrpLeuProGlnGluThrLeuGluLeuSerGlySerArgLeu 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db        901 GTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAACCCTGGAGCTGTCGGGAAGCAAATTG 960

Qy        336 GluGln 337
              ||||||
Db        961 GAGCAG 966

RESULT 2
US-09-254-227A-6
; Sequence 6, Application US/09254227A
; Patent No. 6696257
; GENERAL INFORMATION:
;  APPLICANT:  Ahmad, Sultan
;  APPLICANT:  Ranville, Denis
;  APPLICANT:  Fortin, Yves
;  APPLICANT:  Lembo, Paola
;  APPLICANT:  O'Donnell, Dajan
;  APPLICANT:  Shi-Hsiang, Shen
;  TITLE OF INVENTION:  G Protein-Coupled Receptors from the Rat and Human
;  FILE REFERENCE:  81823/268117
;  CURRENT APPLICATION NUMBER: US/09/254,227A
;  CURRENT FILING DATE:  1999-03-03
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 6
;  LENGTH: 969
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-254-227A-6

Alignment Scores:
Pred. No.:                5.5e-153      Length:          969
Score:                    1598.00       Matches:         307
Percent Similarity:       97.20%        Conservative:    5
Best Local Similarity:    95.64%        Mismatches:      9
Query Match:              90.64%        Indels:          0
DB:                       4             Gaps:            0

US-09-867-570-2 (1-337) x US-09-254-227A-6 (1-969)

Qy         16 MetAspSerThrIleProValLeuGlyThrGluLeuThrProIleAsnGlyArgGluGlu 35
              ||||||   |||:::|||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGATCCAACCGTCCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAG 60

Qy         36 ThrProCysTyrLysGlnThrLeuSerPheThrGlyLeuThrCysIleValSerLeuVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCTTGTC 120

Qy         56 AlaLeuThrGlyAsnAlaValValLeuTrpLeuLeuGlyCysArgMetArgArgAsnAla 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTGCCGCATGCGCAGGAACGCT 180

Qy         76 ValSerIleTyrIleLeuAsnLeuValAlaAlaAspPheLeuPheLeuSerGlyHisIle 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTCTCCATCTACATCCTCAACCTGGTCGCGGCCGACTTCCTCTTCCTTAGCGGCCACATT 240

Qy         96 IleCysSerProLeuArgLeuIleAsnIleArgHisProIleSerLysIleLeuSerPro 115
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        241 ATATGTTCGCCGTTACGCCTCATCAATATCAGCCATCCCATCTCCAAAATCCTCAGTCCT 300

Qy        116 ValMetThrPheProTyrPheIleGlyLeuSerMetLeuSerAlaIleSerThrGluArg 135
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db        301 GTGATGACCTTTCCCTACTTTATAGGCCTAAGCATGCTGAACGCCATCAGCACCGAGCGC 360

Qy        136 CysLeuSerIleLeuTrpProIleTrpTyrHisCysArgArgProArgTyrLeuSerSer 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCGCCCCAGATACCTGTCATCG 420

Qy        156 ValMetCysValLeuLeuTrpAlaLeuSerLeuLeuArgSerIleLeuGluTrpMetPhe 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCATGTGTGTCCTGCTCTGGGCCCCGTCCCTGCTGCGGAGTATCCTGGAGTGGATGTTC 480

Qy        176 CysAspPheLeuPheSerGlyAlaAspSerValTrpCysGluThrSerAspPheIleThr 195
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        481 TGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTCGGTGTGAAACGTCAGATTTCATTACA 540

Qy        196 IleAlaTrpLeuValPheLeuCysValValLeuCysGlySerSerLeuValLeuLeuVal 215
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        541 ATCGCGTGGCTGGTTTTTTTACGTGTGGTTCTCTGTGGGTCCAGCCTGGTCCTGCTGGTC 600

Qy        216 ArgIleLeuCysGlySerArgLysMetProLeuThrArgLeuTyrValThrIleLeuLeu 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCCTCCTC 660

Qy        236 ThrValLeuValPheLeuLeuCysGlyLeuProPheGlyIleGlnTrpAlaLeuPheSer 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACAGTGCTGGTCTTCCTCCTCTGTGGCCTGCCCTTTGGCATTCAGTGGGCCCTGTTTTCC 720
```

Query Match: 97.62% Indels: 0
DB: 15 Gaps: 0

US-09-867-570-2 (1-337) x US-10-225-567A-673 (1-1400)

```
Qy          6 SerTrpValIleArgLeuGlyPheLeuSerMetAspSerThrIleProValLeuGlyThr 25
              |||  |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 TCCAGGGTCACCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACA 361

Qy         26 GluLeuThrProIleAsnGlyArgGluGluThrProCysTyrLysGlnThrLeuSerPhe 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GAACTGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTC 421

Qy         46 ThrGlyLeuThrCysIleValSerLeuValAlaLeuThrGlyAsnAlaValValLeuTrp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 ACGGGGCTGACGTGCATCGTTTCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGCTCTGG 481

Qy         66 LeuLeuGlyCysArgMetArgArgAsnAlaValSerIleTyrIleLeuAsnLeuValAla 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 CTCCTGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCG 541

Qy         86 AlaAspPheLeuPheLeuSerGlyHisIleIleCysSerProLeuArgLeuIleAsnIle 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GCCGACTTCCTCTTCCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCATCAATATC 601

Qy        106 ArgHisProIleSerLysIleLeuSerProValMetThrPheProTyrPheIleGlyLeu 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CGCCATCCCATGTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCTACTTTATAGGCCTA 661

Qy        126 SerMetLeuSerAlaIleSerThrGluArgCysLeuSerIleLeuTrpProIleTrpTyr 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 AGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTAC 721

Qy        146 HisCysArgArgProArgTyrLeuSerSerValMetCysValLeuLeuTrpAlaLeuSer 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 CACTGCCGCCGCCCCAGATACCTGTCATCGGTCATGTGTGTCCTGCTCTGGGCCCTGTCC 781

Qy        166 LeuLeuArgSerIleLeuGluTrpMetPheCysAspPheLeuPheSerGlyAlaAspSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 CTGCTGCGGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTCT 841

Qy        186 ValTrpCysGluThrSerAspPheIleThrIleAlaTrpLeuValPheLeuCysValVal 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 GTTTGGTGTGAAACGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTTATGTGTGGTT 901

Qy        206 LeuCysGlySerSerLeuValLeuLeuValArgIleLeuCysGlySerArgLysMetPro 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 CTCTGTGGGTCCAGCCTGGTCCTGCTGGTCAGGATTCTCTGTGGATCCCGGAAGATGCCG 961

Qy        226 LeuThrArgLeuTyrValThrIleLeuLeuThrValLeuValPheLeuLeuCysGlyLeu 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 CTGACCAGGCTGTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCCTCTGTGGCCTG 1021

Qy        246 ProPheGlyIleGlnTrpAlaLeuPheSerArgIleHisLeuAspTrpLysValLeuPhe 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 CCCTTTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTT 1081

Qy        266 CysHisValHisLeuValSerIlePheLeuSerAlaLeuAsnSerSerAlaAsnProIle 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 TGTCATGTGCATCTAGTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCATC 1141

Qy        286 IleTyrPhePheValGlySerPheArgGlnArgGlnAsnArgGlnAsnLeuLysLeuVal 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 ATTTACTTCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTT 1201

Qy        306 LeuGlnArgAlaLeuGlnAspThrProGluValAspGluGlyGlyGlyTrpLeuProGln 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 CTCCAGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAG 1261

Qy        326 GluThrLeuGluLeuSerGlySerArgLeuGluGln 337
              |||||||||||||||||||||||||||||||||||
Db       1262 GAAACCCTGGAGCTGTCGGGAAGCAGATTGGAGCAG 1297
```

RESULT 6
US-09-995-225-19
; Sequence 19, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-19

Alignment Scores:

Pred. No.:	2.99e-168	Length:	969
Score:	1688.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.75%	Indels:	0
DB:	9	Gaps:	0

US-09-867-570-2 (1-337) x US-09-995-225-19 (1-969)

```
Qy         16 MetAspSerThrIleProValLeuGlyThrGluLeuThrProIleAsnGlyArgGluGlu 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAG 60

Qy         36 ThrProCysTyrLysGlnThrLeuSerPheThrGlyLeuThrCysIleValSerLeuVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCTTGTC 120

Qy         56 AlaLeuThrGlyAsnAlaValValLeuTrpLeuLeuGlyCysArgMetArgArgAsnAla 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTGCCGCATGCGCAGGAACGCT 180

Qy         76 ValSerIleTyrIleLeuAsnLeuValAlaAlaAspPheLeuPheLeuSerGlyHisIle 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        181 GTCTCCATCTACATCCTCAACCTGGTCGCGGCCGACTTCCTCTTCCTTAGCGGCCACATT 240

Qy         96 IleCysSerProLeuArgLeuIleAsnIleArgHisProIleSerLysIleLeuSerPro 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATATGTTCGCCGTTACGCCTCATCAATATCCGCCATCCCATCTCCAAAATCCTCAGTCCT 300

Qy        116 ValMetThrProTyrPheIleGlyLeuSerMetLeuSerAlaIleSerThrGluArg 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGATGACCTTTCCCTACTTTATAGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGC 360

Qy        136 CysLeuSerIleLeuTrpProIleTrpTyrHisCysArgArgProArgTyrLeuSerSer 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCGCCCCAGATACCTGTCATCG 420

Qy        156 ValMetCysValLeuLeuTrpAlaLeuSerLeuLeuArgSerIleLeuGluTrpMetPhe 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCATGTGTGTCCTGCTCTGGGCCCTGTCCCTGCTGCGGAGTATCCTGGAGTGGATGTTC 480

Qy        176 CysAspPheLeuPheSerGlyAlaAspSerValTrpCysGluThrSerAspPheIleThr 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTTGGTGTGAAACGTCAGATTTCATTACA 540

Qy        196 IleAlaTrpLeuValPheLeuCysValValLeuCysGlySerSerLeuValLeuLeuVal 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCGCGTGGCTGGTTTTTTTATGTGTGGTTCTCTGTGGGTCCAGCCTGGTCCTGCTGGTC 600

Qy        216 ArgIleLeuCysGlySerArgLysMetProLeuThrArgLeuTyrValThrIleLeuLeu 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCCTCCTC 660

Qy        236 ThrValLeuValPheLeuLeuCysGlyLeuProPheGlyIleGlnTrpAlaLeuPheSer 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACAGTGCTGGTCTTCCTCCTCTGTGGCCTGCCCTTTGGCATTCAGTGGGCCCTGTTTTCC 720

Qy        256 ArgIleHisLeuAspTrpLysValLeuPheCysHisValHisLeuValSerIlePheLeu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTTCCATTTTCCTG 780

Qy        276 SerAlaLeuAsnSerSerAlaAsnProIleIleTyrPhePheValGlySerPheArgGln 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCCGCTCTTAACAGCAGTGCCAACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG 840

Qy        296 ArgGlnAsnArgGlnAsnLeuLysLeuValLeuGlnArgAlaLeuGlnAspThrProGlu 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGGACACGCCTGAG 900

Qy        316 ValAspGluGlyGlyGlyTrpLeuProGlnGluThrLeuGluLeuSerGlySerArgLeu 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAACCCTGGAGCTGTCGGGAAGCAGATTG 960

Qy        336 GluGln 337
              ||||||
Db        961 GAGCAG 966

RESULT 7
US-09-995-225-19
; Sequence 19, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
;  APPLICANT: Chen, Ruoping
;  APPLICANT:  Chu, Zhi Liang
;  APPLICANT:  Dang, Huong T.
;  APPLICANT: Lowitz, Kevin P.
;  APPLICANT:  Pride, Cameron
;  TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0308
;  CURRENT APPLICATION NUMBER: US/09/995,225
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  PRIOR APPLICATION NUMBER: PCT/US99/23938
;  PRIOR FILING DATE: 1998-10-13
;  PRIOR APPLICATION NUMBER: 60/253,404
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/255,366
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: 60/270,286
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/282,365
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/270,266
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/282,032
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/282,358
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/282,356
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/290,917
;  PRIOR FILING DATE: 2001-05-14
;  PRIOR APPLICATION NUMBER: 60/309,208
;  PRIOR FILING DATE: 2001-07-31
;  NUMBER OF SEQ ID NOS: 67
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;  LENGTH: 969
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-19

Alignment Scores:
Pred. No.:                2.99e-168       Length:          969
Score:                    1688.00         Matches:         322
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              95.76%          Indels:          0
DB:                       10              Gaps:            0

US-09-867-570-2 (1-337) x US-09-995-225-19 (1-969)

Qy         16 MetAspSerThrIleProValLeuGlyThrGluLeuThrProIleAsnGlyArgGluGlu 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAG 60

Qy         36 ThrProCysTyrLysGlnThrLeuSerPheThrGlyLeuThrCysIleValSerLeuVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCTTGTC 120

Qy         56 AlaLeuThrGlyAsnAlaValValLeuTrpLeuLeuGlyCysArgMetArgArgAsnAla 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTGCCGCATGCGCAGGAACGCT 180

Qy         76 ValSerIleTyrIleLeuAsnLeuValAlaAlaAspPheLeuPheLeuSerGlyHisIle 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTCTCCATCTACATCCTCAACCTGGTCGCGGCCGACTTCCTCTTCCTTAGCGGCCACATT 240

Qy         96 IleCysSerProLeuArgLeuIleAsnIleArgHisProIleSerLysIleLeuSerPro 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATATGTTCGCCGTTACGCCTCATCAATATCCGCCATCCCATCTCCAAAATCCTCAGTCCT 300

Qy        116 ValMetThrProTyrPheIleGlyLeuSerMetLeuSerAlaIleSerThrGluArg 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGATGACCTTTCCCTACTTTATAGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGC 360

Qy        136 CysLeuSerIleLeuTrpProIleTrpTyrHisCysArgArgProArgTyrLeuSerSer 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCGCCCCAGATACCTGTCATCG 420

Qy        156 ValMetCysValLeuLeuTrpAlaLeuSerLeuLeuArgSerIleLeuGluTrpMetPhe 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCATGTGTGTCCTGCTCTGGGCCCTGTCCCTGCTGCGGAGTATCCTGGAGTGGATGTTC 480

Qy        176 CysAspPheLeuPheSerGlyAlaAspSerValTrpCysGluThrSerAspPheIleThr 195
```